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**RAW SEQUENCE LISTING**  
**PATENT APPLICATION:** US/09/873,106B

**DATE:** 05/02/2002  
**TIME:** 17:04:59

**Input Set :** A:\10621021004 sub seq.txt  
**Output Set:** N:\CRF3\05022002\I873106B.raw

4 <110> APPLICANT: Reinherz, Ellis L.  
 5 Freund, Christian  
 6 Li, Jing  
 7 Nishizawa, Kazuhisa  
 8 Wagner, Gerhard  
 10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2  
     Binding Protein (CD2BP2)  
 14 <130> FILE REFERENCE: 1062.1021-004  
 16 <140> CURRENT APPLICATION NUMBER: US 09/873,106B  
 17 <141> CURRENT FILING DATE: 2001-06-01  
 19 <150> PRIOR APPLICATION NUMBER: US 60/111,007  
 20 <151> PRIOR FILING DATE: 1998-12-04  
 22 <150> PRIOR APPLICATION NUMBER: US 60/115,647  
 23 <151> PRIOR FILING DATE: 1999-01-13  
 25 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993  
 26 <151> PRIOR FILING DATE: 1999-11-15  
 28 <160> NUMBER OF SEQ ID NOS: 25  
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 1299  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Homo sapiens  
 37 <220> FEATURE:  
 38 <221> NAME/KEY: CDS  
 39 <222> LOCATION: (121)...(1143)  
 41 <400> SEQUENCE: 1  
 42 agtcctcttc cgggtgatgg cggcggtgc cccggatgt agcatctct 60  
 43 tcttttttcc acctcgccctt ccgcggattc ccagcttgag aaacacctct ttgccccgtc 120  
 44 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gat 168  
 45 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Asp  
 46 1                 5                 10                 15  
 48 gag gat gaa atc att gtc ccc aag aag ctg gtg gac cct gtg gct 216  
 49 Glu Asp Glu Ile Ile Val Pro Lys Lys Leu Val Asp Pro Val Ala  
 50                 20                 25                 30  
 52 ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264  
 53 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp  
 54                 35                 40                 45  
 56 agc gat gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312  
 57 Ser Asp Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp  
 58                 50                 55                 60  
 60 atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360  
 61 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
 62 65                 70                 75                 80

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64	agc gag ggg ggt ggt cggt atc aca ccc ttt aac ctg cag gag gag atg	408
65	Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met	
66	85 90 95	
68	gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat	456
69	Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp	
70	100 105 110	
72	gct cag atc cga gac agc tgg ctg gac aac att gac tgg gtg aag atc	504
73	Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile	
74	115 120 125	
76	cgg gag cgg cca cct ggc cag cgc cag gcc tca gac tcg gag gag gag	552
77	Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu	
78	130 135 140	
80	gac agc ttg ggc cag acc tca atg agt gcc caa gcc ctc ttg gag gga	600
81	Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly	
82	145 150 155 160	
84	ctt ttg gag ctc cta ttg cct aga gag aca gtg gct ggg gca ctg agg	648
85	Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg	
86	165 170 175	
88	cgt ctg ggg gcc cga gga gga ggc aaa ggg aga aag ggg cct ggg caa	696
89	Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln	
90	180 185 190	
92	ccc agt tcc cct cag cgc ctg gac cgg ctc tcc ggg ttg gcc gac cag	744
93	Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln	
94	195 200 205	
96	atg gtg gcc cgg ggc aac ctt ggt gtg tac cag gaa aca agg gaa cgg	792
97	Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg	
98	210 215 220	
100	ttg gct atg cgt ctg aag ggt ttg ggg tgt cag acc cta gga ccc cac	840
101	Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His	
102	225 230 235 240	
104	aat ccc aca ccc cca ccc tcc ctg gac atg ttc gct gag gag ttg gcg	888
105	Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala	
106	245 250 255	
108	gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag	936
109	Glu Glu Glu Leu Glu Thr Pro Thr Pro Gln Arg Gly Glu Ala Glu	
110	260 265 270	
112	tgc cgg gga gat ggt ctg gtg gat gtg atg tgg gaa tat aag tgg gag	984
113	Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu	
114	275 280 285	
116	aac acg ggg gat gcc gag ctg tat ggg ccc ttc acc agc gcc cag atg	1032
117	Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met	
118	290 295 300	
120	cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg	1080
121	Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg	
122	305 310 315 320	
124	aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac	1128
125	Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp	
126	325 330 335	
128	ttt gac ctc tac acc tgagcctgct gggggccccag tttgggtgggc ccttcttcc	1183

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129 Phe Asp Leu Tyr Thr  
130 340  
132 tggactttgt ggaggaggca ccaagtgtct cagggcagcga ggaaatttggaa ggccatTTTT 1243  
133 cagtcaattt ccctttccca ataaaagcct tagttgtgta aaaaaaaaaaaaaaaa 1299  
135 <210> SEQ ID NO: 2  
136 <211> LENGTH: 341  
137 <212> TYPE: PRT  
138 <213> ORGANISM: Homo sapiens  
140 <400> SEQUENCE: 2  
141 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp  
142 1 5 10 15  
143 Glu Asp Glu Ile Ile Val Pro Lys Lys Leu Val Asp Pro Val Ala  
144 20 25 30  
145 Gly 'Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp  
146 35 40 45  
147 Ser Asp Glu Glu Asp Asp Asp Gly Ser Ser Lys Tyr Asp  
148 50 55 60  
149 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
150 65 70 75 80  
151 Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met  
152 85 90 95  
153 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp  
154 100 105 110  
155 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile  
156 115 120 125  
157 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu  
158 130 135 140  
159 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly  
160 145 150 155 160  
161 Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg  
162 165 170 175  
163 Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln  
164 180 185 190  
165 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln  
166 195 200 205  
167 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg  
168 210 215 220  
169 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His  
170 225 230 235 240  
171 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala  
172 245 250 255  
173 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu  
174 260 265 270  
175 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu  
176 275 280 285  
177 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met  
178 290 295 300  
179 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg  
180 305 310 315 320

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181 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp  
182 325 330 335  
183 Phe Asp Leu Tyr Thr  
184 340  
187 <210> SEQ ID NO: 3  
188 <211> LENGTH: 26  
189 <212> TYPE: PRT  
190 <213> ORGANISM: Homo sapiens  
192 <400> SEQUENCE: 3  
193 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr  
194 1 5 10 15  
195 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly  
196 20 25  
199 <210> SEQ ID NO: 4  
200 <211> LENGTH: 27  
201 <212> TYPE: PRT  
202 <213> ORGANISM: Caenorhabditis elegans  
204 <400> SEQUENCE: 4  
205 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu  
206 1 5 10 15  
207 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly  
208 20 25  
211 <210> SEQ ID NO: 5  
212 <211> LENGTH: 27  
213 <212> TYPE: PRT  
214 <213> ORGANISM: Caenorhabditis elegans  
216 <400> SEQUENCE: 5  
217 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn  
218 1 5 10 15  
219 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu  
220 20 25  
223 <210> SEQ ID NO: 6  
224 <211> LENGTH: 27  
225 <212> TYPE: PRT  
226 <213> ORGANISM: Caenorhabditis elegans  
228 <400> SEQUENCE: 6  
229 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu  
230 1 5 10 15  
231 Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn  
232 20 25  
235 <210> SEQ ID NO: 7  
236 <211> LENGTH: 29  
237 <212> TYPE: PRT  
238 <213> ORGANISM: Saccharomyces cerevisiae  
240 <400> SEQUENCE: 7  
241 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser  
242 1 5 10 15  
243 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr  
244 20 25

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Input Set : A:\10621021004 sub seq.txt  
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247 <210> SEQ ID NO: 8  
248 <211> LENGTH: 27  
249 <212> TYPE: PRT  
250 <213> ORGANISM: *Saccharomyces cerevisiae*  
252 <400> SEQUENCE: 8  
253 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser  
254 1 5 10 15  
255 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr  
256 20 25  
259 <210> SEQ ID NO: 9  
260 <211> LENGTH: 17  
261 <212> TYPE: PRT  
262 <213> ORGANISM: Artificial Sequence  
264 <220> FEATURE:  
265 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2  
W--> 268 <221> NAME/KEY: VARIANT  
269 <222> LOCATION: 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14  
270 <223> OTHER INFORMATION: Xaa = Any Amino Acid  
W--> 272 <400> 9  
W--> 273 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr  
274 1 5 10 15  
275 Phe  
279 <210> SEQ ID NO: 10  
280 <211> LENGTH: 6  
281 <212> TYPE: PRT  
282 <213> ORGANISM: Artificial Sequence  
284 <220> FEATURE:  
285 <223> OTHER INFORMATION: CD2BP2 binding region  
288 <400> SEQUENCE: 10  
289 Pro Pro Pro Gly His Arg  
290 1 5  
293 <210> SEQ ID NO: 11  
294 <211> LENGTH: 70  
295 <212> TYPE: PRT  
296 <213> ORGANISM: *Homo sapiens*  
298 <400> SEQUENCE: 11  
299 Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro  
300 1 5 10 15  
301 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro  
302 20 25 30  
303 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro  
304 35 40 45  
305 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser  
306 50 55 60  
307 Leu Ser Pro Ser Ser Asn  
308 65 70  
311 <210> SEQ ID NO: 12  
312 <211> LENGTH: 8  
313 <212> TYPE: DNA